

OIFE

#3

## RAW SEQUENCE LISTING

DATE: 12/06/2001

PATENT APPLICATION: US/09/836,544A

TIME: 12:15:40

Input Set : A:\11-881.app

Output Set: N:\CRF3\12062001\I836544A.raw

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 7 <130> FILE REFERENCE: 11-88L  
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 10 <141> CURRENT FILING DATE: 2001-04-17  
 12 <150> PRIOR APPLICATION NUMBER: US 07/983,647  
 13 <151> PRIOR FILING DATE: 1992-12-01  
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 16 <151> PRIOR FILING DATE: 1990-07-13  
 18 <150> PRIOR APPLICATION NUMBER: US 07/498,809  
 19 <151> PRIOR FILING DATE: 1990-03-23  
 21 <150> PRIOR APPLICATION NUMBER: US 07/379,076  
 22 <151> PRIOR FILING DATE: 1989-07-13  
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 25 <151> PRIOR FILING DATE: 1988-02-25  
 27 <160> NUMBER OF SEQ ID NOS: 37  
 29 <170> SOFTWARE: PatentIn Ver. 2.0  
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 36 <220> FEATURE:  
 37 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleotide  
 38 sequence of expression vector, pIH3  
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 45 atactgtcct tctagtgtag ccgtagttag gccaccactt caagaactct gtagcaccgc 180  
 47 ctacatacct cgctctgcta atcctgttac cagtggctgc tgccagtggc gataagtgt 240  
 49 gtcttaccgg gttggactca agacgatagt taccggataa ggcgcagcgg tcgggctgaa 300  
 51 cggggggttc gtgcacacag cccagcttgg agcgaacgac ctacaccgaa ctgagatacc 360  
 53 tacagcgtga gctatgagaa agcggcacgc ttcccgaagg gagaaaggcg gacaggatc 420  
 55 cgtaagcgg cagggtcgga acagggagagc gcacgaggga gcttccaggg ggaaacgcct 480  
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 61 tctcaacgta aacttttaca gcggcgcgctc atttgatatg atgcgccccg cttcccgata 660  
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 65 gactctaaat ctgccgtcat cgacttcgaa ggttcgaatc cttccccac caccatcact 780  
 67 ttcaaaaagtc cgaaagaatc tgctccctgc ttgtgtgttg gaggtcgtg agtagtgccg 840  
 69 gagtaaaatt taagctacaa caaggcaagg cttgaccgac aattgcatga agaattctgt 900  
 71 tagggtagg cgttttgcgc tgcttcgcga tgtacggggc agatatacgc gttgacattg 960  
 73 attattgact agttattaat agtaatcaat tacgggggtca ttagttcata gcccatatat 1020  
 75 ggagtccgc gttacataac ttacggtaaa tggcccgcct ggctgaccgc ccaacgacct 1080  
 77 ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag ggactttcca 1140  
 79 ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtag atcaagtgt 1200  
 81 tcatatgcca agtacgcccc ctattgacgt caatgacggg aaatggcccg cctggcatta 1260  
 83 tgcccagtag atgaccttat gggactttcc tacttggcag tacatctacg tattagtcac 1320

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89 aaatcaacgg gactttccaa aatgtcgtaa caactccgcc ccattgacgc aaatgggcg 1500
91 aattcctggg cgggactggg gagtggcgag ccctcagatg ctgcatataa gcagctgctt 1560
93 tttgctgtga ctgggtctct ctggttagac cagatctgag cctgggagct ctctggctaa 1620
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97 tcttccatac ctaccagttc tgcgccgtgca ggtcgcggcc gcgactctag aggatctttg 1740
99 tgaaggaaacc ttacttctgt ggtgtgacat aattggacaa actacctaca gagatttaaa 1800
101 gctctaaggt aaatataaaa tttttaagtg tataatgtgt taaactactg attctaattg 1860
103 tttgtgtatt ttagattcca acctatggaa ctgatgaatg ggagcagtgg tggaatgcct 1920
105 ttaatgagga aaacctgttt tgctcagaag aaatgccatc tagtgatgat gaggctactg 1980
107 ctgactctca acattctact cctccaaaaa agaagagaaa ggtagaagac cccaaggact 2040
109 ttccttcaga attgctaagt tttttgagtc atgctgtgtt tagtaataga actcttgctt 2100
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113 aatattctgt aacctttata agtaggcata acagttataa tcataacata ctgttttttc 2220
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117 ttagcttttt aatttgtaaa ggggttaata aggaatattt gatgtatagt gccttgacta 2340
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129 agtatgcaaa gcatgcatct caattagtc gcaaccaggt gtggaaagtc cccaggctcc 2700
131 ccagcaggca gaagtatgca aagcatgcat ctcaattagt cagcaaccat agtcccgc 2760
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135 tgactaattt tttttattta tgcagaggcc gaggcgcgct cggcctctga gctattccag 2880
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145 &lt;220&gt; FEATURE:

146 &lt;221&gt; NAME/KEY: CDS

147 &lt;222&gt; LOCATION: (7)..(1059)

149 &lt;400&gt; SEQUENCE: 2

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151 Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile
152 1 5 10
154 ttc aat gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc 96
155 Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala
156 15 20 25 30
158 ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct 144
159 Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro
160 35 40 45
162 agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act 192
163 Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr
164 50 55 60
166 tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc 240
167 Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe

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170	aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att	288		
171	Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile			
172	80	85	90	
174	aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat	336		
175	Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr			
176	95	100	105	110
178	gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att	384		
179	Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile			
180	115	120	125	
182	caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca	432		
183	Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr			
184	130	135	140	
186	acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg	480		
187	Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu			
188	145	150	155	
190	tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac	528		
191	Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His			
192	160	165	170	
194	aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac	576		
195	Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn			
196	175	180	185	190
198	aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa	624		
199	Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys			
200	195	200	205	
202	ggg ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc	672		
203	Gly Leu Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu			
204	210	215	220	
206	ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa	720		
207	Leu Met Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys			
208	225	230	235	
210	aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac	768		
211	Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His			
212	240	245	250	
214	aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct	816		
215	Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala			
216	255	260	265	270
218	tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct	864		
219	Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro			
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222	ggg cat cgt tcc cag gca cct agt cat cgt ccc ccg cct cct gga cac	912		
223	Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His			
224	290	295	300	
226	cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tcg ggc aca	960		
227	Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr			
228	305	310	315	
230	caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag	1008		
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232	320	325	330	

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238 aat taaaaaagat agaaactgtc tttttcaata aaaagcactg tggatttctg 1109
239 Asn
241 ccctcctgat gtgcatatcc gtacttccat gaggtgtttt ctgtgtgcag aacattgtca 1169
243 cctcctgagg ctgtgggcca cagccacctc tgcattctcg aactcagcca tgtgggtcaac 1229
245 atctggagtt tttggtctcc tcagagagct ccatcacacc agtaaggaga agcaatataa 1289
247 gtgtgattgc aagaatggta gaggaccgag cacagaaatc ttagagattt cttgtcccct 1349
249 ctcagggtcat gtgtagatgc gataaatcaa gtgattggtg tgcctgggtc tcactacaag 1409
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258 <212> TYPE: PRT
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266 20 25 30
268 Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
269 35 40 45
271 Gln Met Ser Asp Asp Ile Asp Ile Lys Trp Glu Lys Thr Ser Asp
272 50 55 60
274 Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
275 65 70 75 80
277 Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
278 85 90 95
280 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
281 100 105 110
283 Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
284 115 120 125
286 Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
287 130 135 140
289 Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
290 145 150 155 160
292 Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
293 165 170 175
295 Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
296 180 185 190
298 Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
299 195 200 205
301 Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
302 210 215 220
304 Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
305 225 230 235 240
307 Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
308 245 250 255

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310 Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
311          260          265          270
313 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His
314          275          280          285
316 Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
317          290          295          300
319 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
320 305          310          315          320
322 His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
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330 <211> LENGTH: 874
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332 <213> ORGANISM: Homo sapiens
334 <220> FEATURE:
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336 <222> LOCATION: (13)..(723)
338 <400> SEQUENCE: 4
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341          1          5          10
343 ctc agc gtg gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt 99
344 Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe
345          15          20          25
347 tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta 147
348 Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
349 30          35          40          45
351 cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat 195
352 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
353          50          55          60
355 aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt 243
356 Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe
357          65          70          75
359 aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac 291
360 Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr
361          80          85          90
363 aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat 339
364 Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn
365          95          100          105
367 att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca 387
368 Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro
369 110          115          120          125
371 tct ccc aca cta act tgt gca ttg act aat gga agc att gaa gtc caa 435
372 Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln
373          130          135          140
375 tgc atg ata cca gag cat tac aac agc cat cga gga ctt ata atg tac 483
376 Cys Met Ile Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr

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VERIFICATION SUMMARY

DATE: 12/06/2001

PATENT APPLICATION: US/09/836,544A

TIME: 12:15:41

Input Set : A:\11-881.app

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OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/836,544

DATE: 12/06/2001  
 TIME: 10:11:02

Input Set : A:\11-88L.txt  
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Does Not Comply  
 Corrected Diskette Needed

3 <110> APPLICANT: The General Hospital Corporation  
 5 <120> TITLE OF INVENTION: Rapid Immunoselection Cloning Method  
 7 <130> FILE REFERENCE: 11-88L  
 9 <140> CURRENT APPLICATION NUMBER: US 09/836,544  
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 27 <160> NUMBER OF SEQ ID NOS: 37  
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/836,544

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